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RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/455,486
 DATE: 02/05/2001
 TIME: 13:12:57

Input Set : A:\129.17-US-11 SEQLIST - 2000-01-12.TXT
 Output Set: N:\CRF3\02052001\1455486.raw

4 <110> APPLICANT: Daniel E. Afar
 5 Rene S. Hubert
 6 Arthur B. Raitano
 7 Douglas C. Saffran
 8 Stephen C. Mitchell
 10 <120> TITLE OF INVENTION: NOVEL SERPENTINE TRANSMEMBRANE ANTIGENS
 11 EXPRESSED IN HUMAN CANCERS AND USES THEREOF
 14 <130> FILE REFERENCE: 129.17-US-11
 16 <140> CURRENT APPLICATION NUMBER: 09/455,486
 17 <141> CURRENT FILING DATE: 1999-12-06
 19 <150> PRIOR APPLICATION NUMBER: 09/323,873
 20 <151> PRIOR FILING DATE: 1999-06-01
 22 <160> NUMBER OF SEQ ID NOS: 34
 24 <170> SOFTWARE: FastSEQ for Windows Version 4.0
 26 <210> SEQ ID NO: 1
 27 <211> LENGTH: 1193
 28 <212> TYPE: DNA
 29 <213> ORGANISM: Homo sapiens
 31 <220> FEATURE:
 32 <221> NAME/KEY: CDS
 33 <222> LOCATION: (64)...(1083)
 35 <400> SEQUENCE: 1
 36 gagactcaag gtcaagctaa gggaagagt ggggtgctga agccatacta ttttatagaa 60
 37 tta atg gaa agc aga aaa gac atc aca aac caa gaa gaa ctt tgg aaa 108
 38 Met Glu Ser Arg Lys Asp Ile Thr Asn Gln Glu Glu Leu Trp Lys
 39 1 5 10 15
 41 atg aag cct agg aga aat tta gaa gaa gac gat tat ttg cat aag gac 156
 42 Met Lys Pro Arg Arg Asn Leu Glu Glu Asp Asp Tyr Leu His Lys Asp
 43 20 25 30
 45 acg gga gag acc agc atg cta aaa aga cct gtg ctt ttg cat ttg cac 204
 46 Thr Gly Glu Thr Ser Met Leu Lys Arg Pro Val Leu Leu His Leu His
 47 35 40 45
 49 caa aca gcc cat gct gat gaa ttt gac tgc cct tca gaa ctt cag cac. 252
 50 Gln Thr Ala His Ala Asp Glu Phe Asp Cys Pro Ser Glu Leu Gln His
 51 50 55 60
 53 aca cag gaa ctc ttt cca cag tgg cac ttg cca att aaa ata gct gct 300
 54 Thr Gln Glu Leu Phe Pro Gln Trp His Leu Pro Ile Lys Ile Ala Ala
 55 65 70 75
 57 att ata gca tct ctg act ttt ctt tac act ctt ctg agg gaa gta att 348
 58 Ile Ile Ala Ser Leu Thr Phe Leu Tyr Thr Leu Leu Arg Glu Val Ile
 59 80 85 90 95
 61 cac cct tta gca act tcc cat caa caa tat ttt tat aaa att cca atc 396
 62 His Pro Leu Ala Thr Ser His Gln Gln Tyr Phe Tyr Lys Ile Pro Ile
 63 100 105 110
 65 ctg gtc atc aac aaa gtc ttg cca atg gtt tcc atc act ctc ttg gca 444
 66 Leu Val Ile Asn Lys Val Leu Pro Met Val Ser Ile Thr Leu Leu Ala
 67 115 120 125

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69 ttg gtt tac ctg cca ggt gtg ata gca gca att gtc caa ctt cat aat      492
70 Leu Val Tyr Leu Pro Gly Val Ile Ala Ala Ile Val Gln Leu His Asn
71      130      135      140
73 gga acc aag tat aag aag ttt cca cat tgg ttg gat aag tgg atg tta      540
74 Gly Thr Lys Tyr Lys Lys Phe Pro His Trp Leu Asp Lys Trp Met Leu
75      145      150      155
77 aca aga aag cag ttt ggg ctt ctc agt ttc ttt ttt gct gta ctg cat      588
78 Thr Arg Lys Gln Phe Gly Leu Leu Ser Phe Phe Phe Ala Val Leu His
79 160      165      170      175
81 gca att tat agt ctg tct tac cca atg agg cga tcc tac aga tac aag      636
82 Ala Ile Tyr Ser Leu Ser Tyr Pro Met Arg Arg Ser Tyr Arg Tyr Lys
83      180      185      190
85 ttg cta aac tgg gca tat caa cag gtc caa caa aat aaa gaa gat gcc      684
86 Leu Leu Asn Trp Ala Tyr Gln Gln Val Gln Gln Asn Lys Glu Asp Ala
87      195      200      205
89 tgg att gag cat gat gtt tgg aga atg gag att tat gtg tct ctg gga      732
90 Trp Ile Glu His Asp Val Trp Arg Met Glu Ile Tyr Val Ser Leu Gly
91      210      215      220
93 att gtg gga ttg gca ata ctg gct ctg ttg gct gtg aca tct att cca      780
94 Ile Val Gly Leu Ala Ile Leu Ala Leu Leu Ala Val Thr Ser Ile Pro
95      225      230      235
97 tct gtg agt gac tct ttg aca tgg aga gaa ttt cac tat att cag agc      828
98 Ser Val Ser Asp Ser Leu Thr Trp Arg Glu Phe His Tyr Ile Gln Ser
99 240      245      250      255
101 aag cta gga att gtt tcc ctt cta ctg ggc aca ata cac gca ttg att      876
102 Lys Leu Gly Ile Val Ser Leu Leu Leu Gly Thr Ile His Ala Leu Ile
103      260      265      270
105 ttt gcc tgg aat aag tgg ata gat ata aaa caa ttt gta tgg tat aca      924
106 Phe Ala Trp Asn Lys Trp Ile Asp Ile Lys Gln Phe Val Trp Tyr Thr
107      275      280      285
109 cct cca act ttt atg ata gct gtt ttc ctt cca att gtt gtc ctg ata      972
110 Pro Pro Thr Phe Met Ile Ala Val Phe Leu Pro Ile Val Val Leu Ile
111      290      295      300
113 ttt aaa agc ata cta ttc ctg cca tgc ttg agg aag aag ata ctg aag      1020
114 Phe Lys Ser Ile Leu Phe Leu Pro Cys Leu Arg Lys Lys Ile Leu Lys
115      305      310      315
117 att aga cat ggt tgg gaa gac gtc acc aaa att aac aaa act gag ata      1068
118 Ile Arg His Gly Trp Glu Asp Val Thr Lys Ile Asn Lys Thr Glu Ile
119 320      325      330      335
121 tgt tcc cag ttg tag aattactggt tacacacatt ttgtttcaat attgatatat      1123
122 Cys Ser Gln Leu *
125 ttatcacca acatttcaag ttgtatttg ttaataaaat gattattcaa ggaaaaaaa      1183
126 aaaaaaaaaa      1193
128 <210> SEQ ID NO: 2
129 <211> LENGTH: 339
130 <212> TYPE: PRT
131 <213> ORGANISM: Homo sapiens
133 <400> SEQUENCE: 2
134 Met Glu Ser Arg Lys Asp Ile Thr Asn Gln Glu Glu Leu Trp Lys Met

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RAW SEQUENCE LISTING DATE: 02/05/2001
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Input Set : A:\129.17-US-I1 SEQLIST - 2000-01-12.TXT
 Output Set: N:\CRF3\02052001\I455486.raw

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135 1          5          10          15
136 Lys Pro Arg Arg Asn Leu Glu Glu Asp Asp Tyr Leu His Lys Asp Thr
137          20          25          30
138 Gly Glu Thr Ser Met Leu Lys Arg Pro Val Leu Leu His Leu His Gln
139          35          40          45
140 Thr Ala His Ala Asp Glu Phe Asp Cys Pro Ser Glu Leu Gln His Thr
141          50          55          60
142 Gln Glu Leu Phe Pro Gln Trp His Leu Pro Ile Lys Ile Ala Ala Ile
143 65          70          75          80
144 Ile Ala Ser Leu Thr Phe Leu Tyr Thr Leu Arg Glu Val Ile His
145          85          90          95
146 Pro Leu Ala Thr Ser His Gln Gln Tyr Phe Tyr Lys Ile Pro Ile Leu
147          100         105         110
148 Val Ile Asn Lys Val Leu Pro Met Val Ser Ile Thr Leu Leu Ala Leu
149          115         120         125
150 Val Tyr Leu Pro Gly Val Ile Ala Ala Ile Val Gln Leu His Asn Gly
151          130         135         140
152 Thr Lys Tyr Lys Lys Phe Pro His Trp Leu Asp Lys Trp Met Leu Thr
153 145         150         155         160
154 Arg Lys Gln Phe Gly Leu Leu Ser Phe Phe Ala Val Leu His Ala
155         165         170         175
156 Ile Tyr Ser Leu Ser Tyr Pro Met Arg Arg Ser Tyr Arg Tyr Lys Leu
157         180         185         190
158 Leu Asn Trp Ala Tyr Gln Gln Val Gln Gln Asn Lys Glu Asp Ala Trp
159         195         200         205
160 Ile Glu His Asp Val Trp Arg Met Glu Ile Tyr Val Ser Leu Gly Ile
161         210         215         220
162 Val Gly Leu Ala Ile Leu Ala Leu Leu Ala Val Thr Ser Ile Pro Ser
163 225         230         235         240
164 Val Ser Asp Ser Leu Thr Trp Arg Glu Phe His Tyr Ile Gln Ser Lys
165         245         250         255
166 Leu Gly Ile Val Ser Leu Leu Leu Gly Thr Ile His Ala Leu Ile Phe
167         260         265         270
168 Ala Trp Asn Lys Trp Ile Asp Ile Lys Gln Phe Val Trp Tyr Thr Pro
169         275         280         285
170 Pro Thr Phe Met Ile Ala Val Phe Leu Pro Ile Val Val Leu Ile Phe
171         290         295         300
172 Lys Ser Ile Leu Phe Leu Pro Cys Leu Arg Lys Lys Ile Leu Lys Ile
173 305         310         315         320
174 Arg His Gly Trp Glu Asp Val Thr Lys Ile Asn Lys Thr Glu Ile Cys
175         325         330         335
176 Ser Gln Leu
179 <210> SEQ ID NO: 3
180 <211> LENGTH: 111
181 <212> TYPE: DNA
182 <213> ORGANISM: Homo sapiens
184 <400> SEQUENCE: 3
185 ggcggaggcg gaggcggagg gcgaggggagc gggagcgccg cctggagcgc ggcaggtcat 60
186 attgaacatt ccagataacct atcattactc gatgctgttg ataacagcaa g 111

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 PATENT APPLICATION: US/09/455,486

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Input Set : A:\129.17-US-I1 SEQLIST - 2000-01-12.TXT
 Output Set: N:\CRF3\02052001\I455486.raw

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188 <210> SEQ ID NO: 4
189 <211> LENGTH: 3627
190 <212> TYPE: DNA
191 <213> ORGANISM: Homo sapiens
193 <400> SEQUENCE: 4
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195 gtgggtggct gaagccatc ttttttatag aattaatgga aagcagaana gacalcacaa      120
196 accaagaaga actttggaaa atgaagccta ggagaaatlt agaagaagac gattattttgc      180
197 ataaggacac gggagagacc agcatgctaa aaagacctgt gcttttgcac ttgcacacaa      240
198 cagcccatgc tgaatgaatt gactgccctt cagaacttca gcacacacag gaactctttc      300
199 cacagtggca ctggccaatt aaaatagctg ctattatagc atctctgact ttctcttaca      360
200 ctcttctgag ggaagttaatt ccccccttag caacttccca tcaacaatat ttttataaaa      420
201 ttccaatcct ggtcatcaac aaagtcttgc caatggtttc catcactctc ttggcatttg      480
202 tttacctgcc aggtgtgata gcagcaattg tccaacttca taatggaacc aagtataaga      540
203 agtttccaca ttggttggtt aagtggatgt taacaagaaa gcagtttggg cttctcagtt      600
204 tcttttttgc tgtactgcac gcaatttata gtctgtctta ccaatgagg cgtactctac      660
205 gatacaagtt gctaaactgq qcatatcaac aggtcccaaa aaataaagaa gatgcctgga      720
206 ttgagcatga tgtttggaga atggagattt atgtgtctct ggggaatttg ggaattggca      780
207 tactggctct gttggctgtg acatctattc catctgtgag tgactctttg acatggagag      840
208 aatttccact tatltaggta aataatatat aaaaataccc taagaggtaa atcttcttlt      900
209 tgtgtttatg atatagaata tgttgacttt accccataaa aaataacaaa tgtttttcaa      960
210 cagcaaatgt cttatacttg ttccaattaa taatgtgtct tctgtttgtt tttccctattg      1020
211 cttctaatga ggacaagtgt ttcttagaca taataaagaa gcatataaat attctttgtt      1080
212 tttttttttt tgtttgtttt tttttgtttt gttttgttgt ttttttgaga tgaagtctcy      1140
213 ctctgtttgc catgtctggg tacagtggca cgtctctggc tcaactgcaac ctgcgcctcc      1200
214 tgggttcagg cgaattctctt gctcagcctt cctgagtagc tgggattaca ggcacccatc      1260
215 accatgtcca gctaattttt gtaatttttag tagagacagg gttttcccat gttggccagg      1320
216 ctgtgtctga tctctgacc tcaaatgac cccccacctc ggcctcccaa agtgctggga      1380
217 tgacagttgt gagccaccac actcagcctg ctctttctaa tatgtgaac ttgttagaca      1440
218 atttgetacc catctaattg gatatttttag gaatccaata tgcattggtt attatttctt      1500
219 aaaaaaataa ttcttttacc tgtcacctga atttagtaat gctttttatg ttacacaaact      1560
220 tagcactttc cagaaacaaa aactctctcc ttgaataaat agagttttta tctacaaaag      1620
221 atatgtcagt gtctcatttc aaagctgtgt ttttccagct tacattttat ataactactc      1680
222 acttgaagtt tctaataatt cttgttaatt taaaactatc tcagatttac tgaggtttat      1740
223 cttctgtgtg tagatttatc ataagaagag tgatgtgcca gaatcactct gggatccttg      1800
224 tctgacaaga ttcaaggagc taattttaat tcagtcatga aactgcca ttaccgttta      1860
225 tgggttagaca tctttggaaa ttccacaaag gtcagacatt cgcactatc cctttacat      1920
226 gtccacacgt atactccaac actttattag gcatctgatt agtttggaat gtatgctctc      1980
227 atctgaatta gtccagtgtg gcttagagtt ggtacacat tctcacagaa ttctctaatt      2040
228 ttgtaggttc agcctgataa ccaactggag tcttttggtc tcatataata gctttcttca      2100
229 cacattgtct tgcctgttac acatatgatg aacactgctt tttagacttc attaggaatt      2160
230 taggactgca tcttgacaac tgagcctatt ctactatatg tacaatacct agccataat      2220
231 aggtatacaa tacacatttg gtaaaaacta ttttcaacca atgacatgta tttttcaact      2280
232 agtaacctag aaatgtttca cttaaaatct gagaactggg tacactacaa gttaccttgg      2340
233 agattcatat atgaaaacgc aaacttagct atttgattgt attcactggg acttaagaat      2400
234 gcgcctgaat aattgtgagt tcgattttgt ctggcaggct aatgacctt tccagtaag      2460
235 tgaatagagg tcagaagtcg tataaaagag gtgtttgtcag aacaccgttg agattacata      2520
236 ggtgaacaac taatttttaag caactttatt tgtgtagtga caaagcatcc caatgcaggc      2580
237 tgaatgtttt catcacatct ctggatctct ctattttgtg cagacattga aaaaattgtt      2640

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RAW SEQUENCE LISTING

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Input Set : A:\129.17-US-I1 SEQLIST - 2000-01-12.TXT

Output Set: N:\CRF3\02052001\I455486.raw

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238 catattattt ccatgttate agaattattt atttlttaaa aacataggcc aagttcattc 2700
239 acitcattat tcattttatc aaatcagagt gaatcacalt agtcgccttc acaactgata 2760
240 aagatcactg aagtcaaaat gatttttgcg ataattctca atctacctat atttaattga 2820
241 gaattctaaa tgtacaaatc attgtgttga ttctgcagtg atcctgctat aagtaagact 2880
242 cagtccctga ttttaggtat cctgtgaaaa gcagaattaa gacaaatata caagagacaa 2940
243 agcacaaaaa ataaatatca taaggggatg aacaaaatgg tggagaaaaga gtagacaaag 3000
244 tttttgatca cctgccttca aagaaaagct gtgaattttg ttcacttaga cagcttggag 3060
245 acaagaaatt acccaaaagt aaggtgagga ggataggcaa aaagagcaga aagatgtgaa 3120
246 tggacattgt tgagaaatgt gataggaaaa caatcataga taaaggattt ccaagcaaca 3180
247 gagcatatcc agatgaggtg ggatgggata aactcttatt gaaccaatct tcaccaatct 3240
248 tgtttttctt ttgcagagca agctaggaaat tgtttccctt ctactgggca caatacacgc 3300
249 attgattttt qcctggaata agtggataga tataaaacaa tttgtatggt atacacctcc 3360
250 aacttttatg atagctgttt tcttcccaat tgttgcctg atatttataa gcatactatt 3420
251 cctgccatgc ttgaggaaqa agatactgaa gattagacat ggttgggaag acgtcaccac 3480
252 aattaacaaa actgagatat gttccaggtt gtagaattac tgtttacaca catttttgtt 3540
253 caattattgat atattttatc accaacatct caagtttgta tttgttaata aaatgattat 3600
254 tcaaggaaaa aaaaaaaaaa aaaaaaa 3627
256 <210> SEQ ID NO: 5
257 <211> LENGTH: 2453
258 <212> TYPE: DNA
259 <213> ORGANISM: Homo sapiens
261 <220> FEATURE:
262 <221> NAME/KEY: CDS
263 <222> LOCATION: (355)...(1719)
265 <400> SEQUENCE: 5
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267 gcagccctta gcggcgctc gctgccaaag cggcctccgc gcgcctccct ccttcttct 120
268 cccctggctg ttgcgatcc agcttgggta ggcgggaag cagctggagt gcgaccgca 180
269 cggcagccac cctgcaaccg ccagtcggag gtgcagtcg taggcccctg ccccggggtg 240
270 ggccttggg gagtcgggc cgtcccgag gagctgcaag gctcggcct gcccgcgctg 300
271 gagggcgcgc ggggcgcgga ggaattctt ggtgatctt gaagtgtccg tctc atg 357
272 Met
273 1
275 gaa tca atc tct atg atg gga agc cct aag agc ctt agt gaa act tgt 405
276 Glu Ser Ile Ser Met Met Gly Ser Pro Lys Ser Leu Ser Glu Thr Cys
277 5 10 15
279 tta cct aat ggc ata aat ggt atc aaa gat gca agg aag gtc act gta 453
280 Leu Pro Asn Gly Ile Asn Gly Ile Lys Asp Ala Arg Lys Val Thr Val
281 20 25 30
283 ggt gtg att gga agt gga gat ttt gcc aaa tcc ttg acc att cga ctt 501
284 Gly Val Ile Gly Ser Gly Asp Phe Ala Lys Ser Leu Thr Ile Arg Leu
285 35 40 45
287 att aga tgc ggc tat cat gtg gtc ata gga agt aga aat cct aag ttt 549
288 Ile Arg Cys Gly Tyr His Val Val Ile Gly Ser Arg Asn Pro Lys Phe
289 50 55 60 65
291 gct tct gaa ttt ttt cct cat gtg gta gat gtc act cat cat gaa gat 597
292 Ala Ser Glu Phe Phe Pro His Val Val Asp Val Thr His His Glu Asp
293 70 75 80
295 gct ctc aca aaa aca aat ata ata ttt gtt gct ata cac aga gaa cat 645

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FYI:

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/455,486

DATE: 02/05/2001

TIME: 13:12:58

Input Set : A:\129.17-US-11 SEQLIST - 2000-01-12.TXT

Output Set: N:\CRF3\02052001\I455486.raw

L:765 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12
L:768 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12
L:769 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12
L:770 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12
L:771 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12
L:782 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:13
L:782 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:13
L:782 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:13
L:784 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:13
L:784 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:13
M:340 Repeated in SeqNo=13
L:790 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:13
L:790 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:13
L:794 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:13
L:794 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:13
L:796 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:13
L:796 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:13
L:798 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:13
L:798 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:13